



09/833041

~~CoFC~~

PATENT  
Customer No. 22,852  
Attorney Docket No. 6832.0016

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re U.S. Patent No.: 6,994,857 )  
Inventors: )  
Craig A. Rosen and William A. Haseltine )  
Issue Date.: February 7, 2006 )  
For: ALBUMIN FUSION PROTEINS )

**Certificate**  
**MAR 10 2006**  
**of Correction**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

**REQUEST FOR CERTIFICATE OF CORRECTION**

Pursuant to 35 U.S.C. §§ 254 and 255, and 37 C.F.R. §§ 1.322 and 1.323, this is a request for a Certificate of Correction in the above-identified patent. Some of the mistakes identified in the appended Form occurred through the fault of the Patent Office, as clearly disclosed by the records of the application which matured into this patent.

For example, the priority claims to Provisional Application Nos. 60/256,931, filed December 21, 2000; 60/199,384, filed April 25, 2000; and 60/229,358, filed April 12, 2000, were deleted in an Amendment filed June 3, 2004, and a Corrected Filing Receipt reflecting the change was mailed by the PTO on August 11, 2004. However, the issued patent was printed with the priority claims in the title page under item (60).  
03/08/2006 SZENDIEI 00000066 6994857 01 FF 1011 100.00 0P

Furthermore, Applicants cited the Hershfield reference once, and also the Hochuli and Nilsson (1997) references in an Information Disclosure Statement filed May

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18, 2004. The initialized PTO 1449 form was returned to Applicants with the Notice of Allowability dated July 20, 2004. However, the patent issued listing the Hershfield reference twice and omitting the Hochuli and Nilsson (1997) references. The Certificate of Correction corrects these errors.

Additionally, none of the corrections made to SEQ ID NOs in the specification by an Amendment filed on May 18, 2004, were incorporated into the issued patent. Similarly, the issued patent reflects the original Sequence Listing filed rather than the Substitute Sequence Listing submitted on May 18, 2004. The Sequence Listing in the attached Certificate of Correction is identical to the Substitute Sequence Listing filed on May 18, 2004, and is also identical to the computer readable copy of the Substitute Sequence Listing also submitted on May 18, 2004. Thus, the correction contains no new matter.

Claims 1(c), 1(i), and claim 22 contain clerical or typographical errors of minor character that are also the result of the Patent Office. Other mistakes identified in the appended Form are of a clerical or typographical nature, or of minor character, and resulted from an error made in good faith by Patentees.

A check in the amount of \$100 (the fee set forth in 37 C.F.R. § 1.20(a)) is attached. Should a check not be appended or should any additional fees be needed, authorization is hereby given to charge any fees due in connection with the filing of this request to Deposit Account No. 06-0916.

Two (2) copies of PTO Form 1050 are appended. The complete Certificate of Correction involves forty-six (46) pages. Issuance of the Certificate of Correction containing the correction is earnestly requested.

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Please charge any required fees not included herewith to our deposit account

06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.

Dated: March 7, 2006

By: Charles E. Van Horn  
Charles E. Van Horn  
Reg. No. 40,266

**UNITED STATES PATENT AND TRADEMARK OFFICE**  
**CERTIFICATE OF CORRECTION**

PATENT NO. 6,994,857 Page 1 of 46  
APPLICATION NO.: 09/833,041  
ISSUE DATE: February 7, 2006  
INVENTOR(S): Craig A. Rosen, William A. Haseltine

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending "provisional application No. 60/256,931, filed on Dec. 1, 2000."

Under item (57) (ABSTRACT) of the title page, "disordrs" should read --disorders--.

On page 7, column 2, in the 8<sup>th</sup> reference, delete the text beginning with "Hershfield, M.S., et al.," to and ending "7185-7189 (1991)" and insert -- Hochuli, E., "Interferon Immunogenicity: Technical Evaluation of Interferon- $\alpha$ 2a," *Journal of Interferon and Cytokine Research* 17:S15-S21 (1997). --

On page 10, column 2, after the 9<sup>th</sup> reference (Nilsson, J., et al.), insert -- Nilsson, J. et al., "Heat-Mediated Activation of Affinity-Immobilized Taq DNA Polymerase," *BioTechniques* 22:744-751 (1997). --

In the Specification:

Col. 25 (Table 1), row HLDOU18, column Exemplary Identifier, "SEQ ID NO:73" should read -- SEQ ID NO:74 --.

Col. 27 (Table 1), row HWACB86, column Exemplary Identifier, "SEQ ID NO:74" should read -- SEQ ID NO:75 --.

Col. 27 (Table 1), row HCEGG08, column Exemplary Identifier, "SEQ ID NO:75" should read -- SEQ ID NO:76 --.

Col. 29 (Table 1), row HWHGZ51, column Exemplary Identifier, "SEQ ID NO:76" should read -- SEQ ID NO:77 --.

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U.S. Patent No. 6,994,857

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Col. 29 (Table 1), row HDTAI21, column Exemplary Identifier, "SEQ ID NO:77" should read -- SEQ ID NO:78 --.

Col. 29 (Table 1), row HCNCA73, column Exemplary Identifier, "SEQ ID NO:78" should read -- SEQ ID NO:79 --.

Col. 29 (Table 1), row HNHFE71, column Exemplary Identifier, "SEQ ID NO:79" should read -- SEQ ID NO:80 --.

Col. 62, lines 38-39, "(SEQ ID NO:36)" should read -- (SEQ ID NO:72) --.

Col. 215, line 8, "(SEQ ID NO:36)" should read -- (SEQ ID NO:81) --.

Col. 236, line 42, "(SEQ ID NO: 37)" should read -- (SEQ ID NO:82) --.

Col. 237, line 47, "(SEQ ID NO:38)" should read -- (SEQ ID NO:83) --.

Col. 237, lines 53-54, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.

Col. 237, line 63, "(SEQ ID NO:40)" should read -- (SEQ ID NO:85) --.

Col. 240, line 55, "(SEQ ID NO:41)" should read -- (SEQ ID NO:86) --.

Col. 240, line 58, "(SEQ ID NO:42)" should read -- (SEQ ID NO:87) --.

Col. 243, line 9, "(SEQ ID NO:43)" should read -- (SEQ ID NO:88) --.

Col. 243, line 14, "(SEQ ID NO:44)" should read -- (SEQ ID NO:89) --.

Col. 243, lines 17-18, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.

Col. 243, line 28, "(SEQ ID NO:45)" should read -- (SEQ ID NO:90) --.

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, beginning with the text "<160> NUMBER OF SEQ ID NOS: 79" to and ending "Pro Thr Ser Cys Ser Arg Cys"  
165

in Col. 313 and insert the following Sequence Listing:

-- <160> NUMBER OF SEQ ID NOS: 90

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

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<220>  
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 <223> primer useful to clone human growth hormone cDNA  
  
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 cccaagaatt cccttatcca ggc 23  
  
 <210> 2  
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 <223> synthetic oligonucleotide used to join DNA fragments  
 with non-cohesive ends.  
  
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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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17

<210> 6

<211> 18

<212> DNA

<213> Artificial Sequence

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<222> 20) .. (24)

<223> first 5 amino acids of mature human serum albumin

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Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys

1

5

10

15

Ile Ser Ala Asp Ala His Lys Ser

20

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<400> 8

gagatgcaca cctgagttag g

21

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<p> &lt;210&gt; 9  &lt;211&gt; 27  &lt;212&gt; DNA  &lt;213&gt; Artificial Sequence  &lt;220&gt;  &lt;221&gt; misc_structure  &lt;223&gt; synthetic oligonucleotide used to join DNA  fragments with non-cohesive ends.    &lt;400&gt; 9  gatcctgtgg cttcgatgca cacaaga </p>	27
<p> &lt;210&gt; 10  &lt;211&gt; 24  &lt;212&gt; DNA  &lt;213&gt; Artificial Sequence  &lt;220&gt;  &lt;221&gt; misc_structure  &lt;223&gt; synthetic oligonucleotide used to join DNA  fragments with non-cohesive ends.    &lt;400&gt; 10  ctcttgtgtg catcgaagcc acag </p>	24
<p> &lt;210&gt; 11  &lt;211&gt; 30  &lt;212&gt; DNA  &lt;213&gt; Artificial Sequence  &lt;220&gt;  &lt;221&gt; misc_structure  &lt;223&gt; synthetic oligonucleotide used to join DNA  fragments with non-cohesive ends.    &lt;400&gt; 11  tgtggaagag cctcagaatt tattcccaac </p>	30
<p> &lt;210&gt; 12  &lt;211&gt; 31  &lt;212&gt; DNA  &lt;213&gt; Artificial Sequence  &lt;220&gt;  &lt;221&gt; misc_structure  &lt;223&gt; synthetic oligonucleotide used to join DNA  fragments with non-cohesive ends.    &lt;400&gt; 12  aattgttggg aataaattct gaggctcttc c </p>	31

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 ac 62

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 <223> synthetic oligonucleotide used to join DNA  
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<400> 16  
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<213> Homo sapiens	
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1 5 10 15	
gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag	96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln	
20 25 30	
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa	144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu	
35 40 45	
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa	192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys	
50 55 60	
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt	240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu	
65 70 75 80	
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct	288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro	
85 90 95	
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc	336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu	
100 105 110	
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat	384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His	
115 120 125	
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga	432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg	
130 135 140	
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	

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tat	aaa	gct	gct	ttt	aca	gaa	tgt	tgc	caa	gct	gct	gat	aaa	gct	gcc	528
Tyr	Lys	Ala	Ala	Phe	Thr	Glu	Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	Ala	
				165					170						175	
tgc	ctg	ttg	cca	aag	ctc	gat	gaa	ctt	cgg	gat	gaa	ggg	aag	gct	tcg	576
Cys	Leu	Leu	Pro	Lys	Leu	Asp	Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	Ser	
			180					185					190			
tct	gcc	aaa	cag	aga	ctc	aaa	tgt	gcc	agt	ctc	caa	aaa	ttt	gga	gaa	624
Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu	
		195					200					205				
aga	gct	ttc	aaa	gca	tgg	gca	gtg	gct	cgc	ctg	agc	cag	aga	ttt	ccc	672
Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro	
	210					215					220					
aaa	gct	gag	ttt	gca	gaa	ggt	tcc	aag	tta	gtg	aca	gat	ctt	acc	aaa	720
Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	
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gtc	cac	acg	gaa	tgc	tgc	cat	gga	gat	ctg	ctt	gaa	tgt	gct	gat	gac	768
Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	
			245					250						255		
agg	gcg	gac	ctt	gcc	aag	tat	atc	tgt	gaa	aat	cag	gat	tcg	atc	tcc	816
Arg	Ala	Asp	Leu	Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	
			260					265					270			
agt	aaa	ctg	aag	gaa	tgc	tgt	gaa	aaa	cct	ctg	ttg	gaa	aaa	tcc	cac	864
Ser	Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	
		275					280					285				
tgc	att	gcc	gaa	gtg	gaa	aat	gat	gag	atg	cct	gct	gac	ttg	cct	tca	912
Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	
	290					295					300					
tta	gct	gct	gat	ttt	gtt	gaa	agt	aag	gat	gtt	tgc	aaa	aac	tat	gct	960
Leu	Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala	
305					310					315					320	
gag	gca	aag	gat	gtc	ttc	ctg	ggc	atg	ttt	ttg	tat	gaa	tat	gca	aga	1008
Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg	
				325				330						335		
agg	cat	cct	gat	tac	tct	gtc	gtg	ctg	ctg	ctg	aga	ctt	gcc	aag	aca	1056
Arg	His	Pro	Asp	Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr	
			340					345					350			
tat	gaa	acc	act	cta	gag	aag	tgc	tgt	gcc	gct	gca	gat	cct	cat	gaa	1104
Tyr	Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	
		355					360					365				

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
370 375 380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	
545 550 555 560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt	1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val	
565 570 575	

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Mar 18 2000

gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag 1782  
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                                   20                                  25                                  30  
  
 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
                                   35                                  40                                  45  
  
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
                                   50                                  55                                  60  
  
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
   65                                  70                                  75                                  80  
  
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
                                   85                                  90                                  95  
  
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
                                   100                                  105                                  110  
  
 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
                                   115                                  120                                  125  
  
 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
   130                                  135                                  140  
  
 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
   145                                  150                                  155                                  160  
  
 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
                                   165                                  170                                  175  
  
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
                                   180                                  185                                  190  
  
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
                                   195                                  200                                  205  
  
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
   210                                  215                                  220

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Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	225	230	235	240
Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	245	250	255	
Arg	Ala	Asp	Leu	Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	260	265	270	
Ser	Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	275	280	285	
Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	290	295	300	
Leu	Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala	305	310	315	320
Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg	325	330	335	
Arg	His	Pro	Asp	Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr	340	345	350	
Tyr	Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	355	360	365	
Cys	Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	370	375	380	
Gln	Asn	Leu	Ile	Lys	Gln	Asn	Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu	385	390	395	400
Tyr	Lys	Phe	Gln	Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro	405	410	415	
Gln	Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys	420	425	430	
Val	Gly	Ser	Lys	Cys	Cys	Lys	His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys	435	440	445	
Ala	Glu	Asp	Tyr	Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His	450	455	460	
Glu	Lys	Thr	Pro	Val	Ser	Asp	Arg	Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	465	470	475	480
Leu	Val	Asn	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	485	490	495	

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Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
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fusion protein in which the albumin moiety is N-terminal  
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Ala

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<400> 39

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<221>primer_bind <223>Degenerate Jkappa reverse primer useful for amplifying human VL domains  <400> 61 acgtttgatc tccagcttgg tccc	24
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<213> Homo sapiens

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Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser
      20              25              30

Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu
      35              40              45

Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val
      50              55              60

Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys
      65              70              75              80

Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr
      85              90              95

Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe
      100             105             110

Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe
      115             120             125

Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln
      130             135             140

Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val
      145             150             155             160

Asp Pro Ser His Asp Leu Lys Gly Ser Val Val Ile Tyr Asp Val Leu
      165             170             175

Asp Gly Thr Asp Ala Trp Asp Ser Ala Thr Glu Thr Lys Thr Phe Leu
      180             185             190

Val Ser Gln Asp Ile Gln Asp Glu Gly Trp Glu Thr Leu Glu Val Ser
      195             200             205

Ser Ala Val Lys Arg Trp Val Arg Ser Asp Ser Thr Lys Ser Lys Asn
      210             215             220

Lys Leu Glu Val Thr Val Glu Ser His Arg Lys Gly Cys Asp Thr Leu
      225             230             235             240

Asp Ile Ser Val Pro Pro Gly Ser Arg Asn Leu Pro Phe Phe Val Val
      245             250             255
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Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu  
260 265 270  
Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser  
275 280 285  
Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr  
290 295 300  
Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser  
305 310 315 320  
Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe  
325 330 335  
Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu  
340 345 350  
Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val  
355 360 365  
Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe  
370 375 380  
Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro  
385 390 395 400  
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405 410 415  
His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg  
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20 25 30  
Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met  
35 40 45  
Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro  
50 55 60

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Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp	Leu	Glu	Val	Asn	Ile	65	70	75	80
Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Ile	85	90	95	
Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His	Cys	Lys	Asp	Gly	Glu	Phe	Arg	100	105	110	
Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys	Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	115	120	125	
Asp	Lys	Glu	Trp	Lys	Ser	Ile	Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	130	135	140	
Gly	Ser	Val	Leu	Met	Ser	Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	145	150	155	160
Trp	Ile	Arg	Thr	Cys	His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	165	170	175	
Val	Trp	Gly	Ser	Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	180	185	190	
Leu	Leu	Leu	Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	195	200	205	
Ser	Lys	Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	210	215	220	
Leu	Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu	225	230	235	240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu	Gly	245	250	255	
Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser	Leu	Gly	260	265	270	
Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser									275	280		

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Phe Arg Leu Pro Arg Lys Trp Gly Trp Arg Thr Glu Ala Thr Ala Pro  
                     20                    25                    30  
 His Ala Pro Val Pro Gln Ser Ile Cys Pro Arg Tyr Thr Ser Pro Cys  
                     35                    40                    45  
 Ala Pro His Asp Cys Gly Ser Gln Thr Val Gln Gly Asn Ser Leu Ser  
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 Leu Phe Tyr Thr Leu Ser His Lys Ala Pro Gln Leu Pro His Arg Val  
                     65                    70                    75                    80  
 Pro Ala Pro Leu Phe Cys Lys Tyr Val Lys Arg Lys Lys Cys Lys Arg  
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 Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys  
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 Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala  
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                     65                    70                    75                    80  
 Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu  
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 His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg  
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 Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly  
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 Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val  
                     130                    135                    140

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Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser  
 145 150 155 160  
 Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn  
 165 170 175  
 Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly  
 180 185 190  
 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly  
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 210 215 220  
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 225 230 235 240  
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 245 250 255  
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 260 265 270  
 Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala  
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 290 295 300  
 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln  
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 Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser  
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                   65                                  70                                  75                                  80  
 Gln Val Cys Asn Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp  
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 Met Leu Arg Lys Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg  
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35 40 45  
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50 55 60  
Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn  
65 70 75 80  
Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln  
85 90 95  
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100 105 110  
Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe  
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<222> (22)  
<223> Xaa equals stop translation

<400> 80  
Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala  
1 5 10 15  
His Ser Gly Arg Ala Xaa  
20  
<210> 81

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```

<211> 733
<212> DNA
<213> Homo sapiens

<400> 81
gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg      60
aattcgaggg tgcaccgtca gtcttcctct tcccccaaa acccaaggac accctcatga      120
tctcccgga tctgaggtc acatgcgtgg tggaggacgt aagccacgaa gacctgagg      180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg      240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact      300
ggctgaatgg caaggagtac aagtgaagg tctccaaca agcctccca acccccatcg      360
agaaaacat ctcaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc      420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct      480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga      540
ccacgcctcc cgtgctggac tccgacggct cttcttctct ctacagcaag ctacaccgtg      600
acaagagcag gtggcagcag gggaaagtct tctcatgctc cgtgatgcat gaggtctctg      660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc      720
gactctagag gat

<210> 82
<211> 5
<212> PRT
<213> Artificial sequence
<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors

<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any

<400> 82
Trp Ser Xaa Trp Ser
  1           5

<210> 83
<211> 86
<212> DNA

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```

<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 83
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc      60
cccgaaatat ctgccatctc aattag                                             86

<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 84
gcggcaagct ttttgcaaag cctaggc                                           27

<210> 85
<211> 271
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 85
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg      60
aaatatctgc catctcaatt agtcagcaac catagtcccc cccctaactc cgcccatccc      120
gccctaact cgcgccagtt cgcgccattc tccgccccat ggctgactaa ttttttttat      180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt      240
ttttggaggc ctaggctttt gcaaaaagct t                                       271

<210> 86
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 86

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gcgctcgagg gatgacagcg atagaacccc gg	32
<210> 87	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<221> primer_bind	
<223> primer useful for generation of a EGR/SEAP reporter construct	
<400> 87	
gcgaagcttc gcgactcccc ggatccgcct c	31
<210> 88	
<211> 12	
<212> DNA	
<213> Artificial Sequence	
<220>	
<221> misc_binding	
<223> NF-KB binding site	
<400> 88	
ggggactttc cc	12
<210> 89	
<211> 73	
<212> DNA	
<213> Artificial Sequence	
<220>	
<221> primer_bind	
<223> forward primer useful for generation of a vector containing the NF-KB promoter element	
<400> 89	
gcggcctcga ggggactttc ccggggactt tccggggact ttcggggact ttccatcctg	60
ccatctcaat tag	73
<210> 90	
<211> 256	
<212> DNA	
<213> Artificial Sequence	
<220>	
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<223> Synthetic NF-KB/SV40 promoter	
<400> 90	
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct	60
caattagtca gcaaccatag tcccgccct aactccgcc atcccgcgcc taactccgcc	120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga	180

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ggccgctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240  
cttttgcaaa aagctt 256  
--.

In the Claims

Col. 313, line 22, in claim 1(c), "amino and" should read -- amino --.

Col. 313, line 33, in claim 1(e), "or fragment thereof and albumin" should read -- or fragment thereof, and albumin --.

Col. 313, line 55, in claim 1(i), "proten" should read -- protein --.

Col. 316, line 17, in claim 22, "protein, or thereof" should read -- protein, or fragment thereof --.

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**UNITED STATES PATENT AND TRADEMARK OFFICE**  
**CERTIFICATE OF CORRECTION**

PATENT NO. 6,994,857

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APPLICATION NO.: 09/833,041

ISSUE DATE: February 7, 2006

INVENTOR(S): Craig A. Rosen, William A. Haseltine

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending "provisional application No. 60/256,931, filed on Dec. 1, 2000."

Under item (57) (ABSTRACT) of the title page, "disordrs" should read --disorders--.

On page 7, column 2, in the 8<sup>th</sup> reference, delete the text beginning with "Hershfield, M.S., et al.," to and ending "7185-7189 (1991)" and insert -- Hochuli, E., "Interferon Immunogenicity: Technical Evaluation of Interferon- $\alpha$ 2a," *Journal of Interferon and Cytokine Research* 17:S15-S21 (1997). --

On page 10, column 2, after the 9<sup>th</sup> reference (Nilsson, J., et al.), insert -- Nilsson, J. et al., "Heat-Mediated Activation of Affinity-Immobilized Taq DNA Polymerase," *BioTechniques* 22:744-751 (1997). --

In the Specification:

Col. 25 (Table 1), row HLD0U18, column Exemplary Identifier, "SEQ ID NO:73" should read -- SEQ ID NO:74 --.

Col. 27 (Table 1), row HWACB86, column Exemplary Identifier, "SEQ ID NO:74" should read -- SEQ ID NO:75 --.

Col. 27 (Table 1), row HCEGG08, column Exemplary Identifier, "SEQ ID NO:75" should read -- SEQ ID NO:76 --.

Col. 29 (Table 1), row HWHGZ51, column Exemplary Identifier, "SEQ ID NO:76" should read -- SEQ ID NO:77 --.

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Col. 29 (Table 1), row HDTAI21, column Exemplary Identifier, "SEQ ID NO:77" should read -- SEQ ID NO:78 --.

Col. 29 (Table 1), row HCNCA73, column Exemplary Identifier, "SEQ ID NO:78" should read -- SEQ ID NO:79 --.

Col. 29 (Table 1), row HNHFE71, column Exemplary Identifier, "SEQ ID NO:79" should read -- SEQ ID NO:80 --.

Col. 62, lines 38-39, "(SEQ ID NO:36)" should read -- (SEQ ID NO:72) --.

Col. 215, line 8, "(SEQ ID NO:36)" should read -- (SEQ ID NO:81) --.

Col. 236, line 42, "(SEQ ID NO: 37)" should read -- (SEQ ID NO:82) --.

Col. 237, line 47, "(SEQ ID NO:38)" should read -- (SEQ ID NO:83) --.

Col. 237, lines 53-54, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.

Col. 237, line 63, "(SEQ ID NO:40)" should read -- (SEQ ID NO:85) --.

Col. 240, line 55, "(SEQ ID NO:41)" should read -- (SEQ ID NO:86) --.

Col. 240, line 58, "(SEQ ID NO:42)" should read -- (SEQ ID NO:87) --.

Col. 243, line 9, "(SEQ ID NO:43)" should read -- (SEQ ID NO:88) --.

Col. 243, line 14, "(SEQ ID NO:44)" should read -- (SEQ ID NO:89) --.

Col. 243, lines 17-18, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.

Col. 243, line 28, "(SEQ ID NO:45)" should read -- (SEQ ID NO:90) --.

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, beginning with the text "<160> NUMBER OF SEQ ID NOS: 79" to and ending "Pro Thr Ser Cys Ser Arg Cys"

165

in Col. 313 and insert the following Sequence Listing:

-- <160> NUMBER OF SEQ ID NOS: 90

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

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<220>	
<221> primer_bind	
<223> primer useful to clone human growth hormone cDNA	
<400> 1	
cccaagaatt cccttatcca ggc	23
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<211> 33	
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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.	
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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 5

ttaggcttat tcccaac

17

<210> 6

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 6

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<210> 7

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> 1)..(19)

<223> invertase leader sequence

<220>

<221> SITE

<222> 20)..(24)

<223> first 5 amino acids of mature human serum albumin

<400> 7

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1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser  
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<210> 8

<211> 21

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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 8

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21

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<210> 9  
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fragments with non-cohesive ends.

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27

<210> 10  
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<220>  
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<210> 11  
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fragments with non-cohesive ends.

<400> 12  
aattgttggg aataaattct gaggtcttcc c

31

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<210> 13  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
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 <223> synthetic oligonucleotide used to join DNA  
 fragments with non-cohesive ends.  
  
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47

<210> 14  
 <211> 48  
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<400> 14  
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48

<210> 15  
 <211> 62  
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 <221> misc\_structure  
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 ac

60  
62

<210> 16  
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 <221> misc\_structure  
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<400> 16  
 aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa

60

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gcc

63

&lt;210&gt; 17

&lt;211&gt; 1782

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1755)

&lt;400&gt; 17

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Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu	
1 5 10 15	
gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag	96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln	
20 25 30	
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa	144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu	
35 40 45	
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa	192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys	
50 55 60	
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt	240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu	
65 70 75 80	
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct	288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro	
85 90 95	
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc	336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu	
100 105 110	
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat	384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His	
115 120 125	
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga	432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg	
130 135 140	
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	

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tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
165 170 175	
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	
180 185 190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu	
195 200 205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro	
210 215 220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys	
225 230 235 240	
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp	
245 250 255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser	
260 265 270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His	
275 280 285	
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Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser	
290 295 300	
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Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala	
305 310 315 320	
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg	
325 330 335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr	
340 345 350	
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa	1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu	
355 360 365	

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
370 375 380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	
545 550 555 560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt	1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val	
565 570 575	

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gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag 1782  
 Ala Ala Ser Gln Ala Ala Leu Gly Leu  
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 <212> PRT  
 <213> Homo Sapiens

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 20 25 30  
 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
 35 40 45  
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 50 55 60  
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 65 70 75 80  
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
 85 90 95  
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
 100 105 110  
 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
 115 120 125  
 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
 130 135 140  
 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
 145 150 155 160  
 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 165 170 175  
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190  
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205  
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
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Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	225	230	235	240
Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	245	250	255	
Arg	Ala	Asp	Leu	Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	260	265	270	
Ser	Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	275	280	285	
Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	290	295	300	
Leu	Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala	305	310	315	320
Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg	325	330	335	
Arg	His	Pro	Asp	Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr	340	345	350	
Tyr	Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	355	360	365	
Cys	Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	370	375	380	
Gln	Asn	Leu	Ile	Lys	Gln	Asn	Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu	385	390	395	400
Tyr	Lys	Phe	Gln	Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro	405	410	415	
Gln	Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys	420	425	430	
Val	Gly	Ser	Lys	Cys	Cys	Lys	His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys	435	440	445	
Ala	Glu	Asp	Tyr	Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His	450	455	460	
Glu	Lys	Thr	Pro	Val	Ser	Asp	Arg	Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	465	470	475	480
Leu	Val	Asn	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	485	490	495	

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Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
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<221> misc\_feature

<222> (55)

<223> n equals a,t,g, or c

<400> 33

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<210> 34

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> signal

<223> Stanniocalcin signal peptide

<400> 34

Met	Leu	Gln	Asn	Ser	Ala	Val	Leu	Leu	Leu	Leu	Val	Ile	Ser	Ala	Ser
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Ala

<210> 35

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<221> signal

<223> Synthetic signal peptide

<400> 35

Met	Pro	Thr	Trp	Ala	Trp	Trp	Leu	Phe	Leu	Val	Leu	Leu	Leu	Ala	Leu
1				5				10						15	

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Trp Ala Pro Ala Arg Gly  
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<210> 36  
<211> 23  
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<221>primer\_bind  
<223>Degenerate VH forward primer useful for  
amplifying human VH domains

<400> 36  
caggtgcagc tgggtgcagtc tgg

23

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<212> DNA  
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amplifying human VH domains

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caggtcaact taaggagtc tgg

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<400> 38  
gaggtgcagc tgggtggagtc tgg

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<210> 39  
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<400> 39

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caggtgcagc tgcaggagtc ggg	23
<210> 40	
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<400> 41	
caggtacagc tgcagcagtc agg	23
<210> 42	
<211> 24	
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<210> 43	
<211> 24	
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tgaagagacg gtgaccattg tccc	24
<210> 44	

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<211> 24  
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 <223>Degenerate Vkappa forward primer useful for  
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 <400> 47  
 gatgttgatga tgactcagtc tcc 23  
  
 <210> 48  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
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<221>primer\_bind  
 <223>Degenerate Vkappa forward primer useful for  
 amplifying human VL domains

<400> 48  
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<210> 49  
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<400> 49  
 gaaattgtgt tgacgcagtc tcc 23

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<400> 50  
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<400> 51  
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<210> 52  
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<400> 52 gaaattgtgc tgactcagtc tcc	23
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<210> 57	

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<221>primer\_bind  
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<400> 61  
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<210> 63  
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cacgttatac tgactcaacc gcc	23
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<210> 71  
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23

<210> 72  
 <211> 15  
 <212> PRT  
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 <221> turn  
 <223> Linker peptide that may be used to join VH  
 and VL domains in an scFv.

<400> 72  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

<210> 73  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 73  
 Cys Cys Cys Ala Ala Gly Ala Ala Thr Thr Cys Cys Cys Thr Thr Ala  
 1 5 10 15

Thr Cys Cys Ala Gly Gly Cys  
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<210> 74  
 <211> 429  
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<213> Homo sapiens

<400> 74

Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu  
1 5 10 15  
Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser  
20 25 30  
Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu  
35 40 45  
Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val  
50 55 60  
Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys  
65 70 75 80  
Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr  
85 90 95  
Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe  
100 105 110  
Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe  
115 120 125  
Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln  
130 135 140  
Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val  
145 150 155 160  
Asp Pro Ser His Asp Leu Lys Gly Ser Val Val Ile Tyr Asp Val Leu  
165 170 175  
Asp Gly Thr Asp Ala Trp Asp Ser Ala Thr Glu Thr Lys Thr Phe Leu  
180 185 190  
Val Ser Gln Asp Ile Gln Asp Glu Gly Trp Glu Thr Leu Glu Val Ser  
195 200 205  
Ser Ala Val Lys Arg Trp Val Arg Ser Asp Ser Thr Lys Ser Lys Asn  
210 215 220  
Lys Leu Glu Val Thr Val Glu Ser His Arg Lys Gly Cys Asp Thr Leu  
225 230 235 240  
Asp Ile Ser Val Pro Pro Gly Ser Arg Asn Leu Pro Phe Phe Val Val  
245 250 255

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Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu  
 260 265 270  
 Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser  
 275 280 285  
 Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr  
 290 295 300  
 Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser  
 305 310 315 320  
 Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe  
 325 330 335  
 Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu  
 340 345 350  
 Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val  
 355 360 365  
 Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe  
 370 375 380  
 Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro  
 385 390 395 400  
 Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr  
 405 410 415  
 His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg  
 420 425

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 <212> PRT  
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 Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu  
 1 5 10 15  
 Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg  
 20 25 30  
 Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met  
 35 40 45  
 Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro  
 50 55 60

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Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp	Leu	Glu	Val	Asn	Ile	65	70	75	80
Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Ile	85	90	95	
Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His	Cys	Lys	Asp	Gly	Glu	Phe	Arg	100	105	110	
Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys	Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	115	120	125	
Asp	Lys	Glu	Trp	Lys	Ser	Ile	Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	130	135	140	
Gly	Ser	Val	Leu	Met	Ser	Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	145	150	155	160
Trp	Ile	Arg	Thr	Cys	His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	165	170	175	
Val	Trp	Gly	Ser	Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	180	185	190	
Leu	Leu	Leu	Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	195	200	205	
Ser	Lys	Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	210	215	220	
Leu	Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu	225	230	235	240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu	Gly	245	250	255	
Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser	Leu	Gly	260	265	270	
Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser									275	280		

<210> 76  
 <211> 112  
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 <213> Homo sapiens

<400> 76  
 Met Phe Trp Val Met Glu Thr Ala Lys Pro Pro Val Ser Glu Asp Ser  
 1 5 10 15

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Phe Arg Leu Pro Arg Lys Trp Gly Trp Arg Thr Glu Ala Thr Ala Pro  
 20 25 30

His Ala Pro Val Pro Gln Ser Ile Cys Pro Arg Tyr Thr Ser Pro Cys  
 35 40 45

Ala Pro His Asp Cys Gly Ser Gln Thr Val Gln Gly Asn Ser Leu Ser  
 50 55 60

Leu Phe Tyr Thr Leu Ser His Lys Ala Pro Gln Leu Pro His Arg Val  
 65 70 75 80

Pro Ala Pro Leu Phe Cys Lys Tyr Val Lys Arg Lys Lys Cys Lys Arg  
 85 90 95

Trp Ser Leu Gly Trp Ser Ser Ser Leu Gln Leu Arg Leu Leu Thr Met  
 100 105 110

<210> 77

<211> 346

<212> PRT

<213> Homo sapiens

<400> 77

Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala  
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Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu  
 20 25 30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys  
 35 40 45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala  
 50 55 60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg  
 65 70 75 80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu  
 85 90 95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg  
 100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly  
 115 120 125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val  
 130 135 140

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Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser  
 145 150 155 160  
 Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn  
 165 170 175  
 Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly  
 180 185 190  
 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly  
 195 200 205  
 Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp  
 210 215 220  
 Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg  
 225 230 235 240  
 Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr  
 245 250 255  
 Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met  
 260 265 270  
 Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala  
 275 280 285  
 Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln  
 290 295 300  
 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln  
 305 310 315 320  
 Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu  
 325 330 335  
 Leu Leu Ala Val Ala Ala Gly Val Leu Leu  
 340 345

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<211> 272

<212> PRT

<213> Homo sapiens

<400> 78

Met Lys Gly Lys Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu  
 1 5 10 15

Asp Glu Asp Ser Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly  
 20 25 30

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Ser Gly Lys Arg Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln  
35 40 45

Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser  
50 55 60

Glu Gln Glu Lys Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu  
65 70 75 80

Gln Val Cys Asn Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp  
85 90 95

Met Leu Arg Lys Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg  
100 105 110

Arg Gly Ala Lys Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly  
115 120 125

Ile Lys Asn Phe Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys  
130 135 140

Thr Ala Gly Pro Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro  
145 150 155 160

Ser Ser Pro Gly Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr  
165 170 175

Thr Val Thr Ala Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val  
180 185 190

Gly Val Gly Gln Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe  
195 200 205

Thr Asp Thr Ser Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro  
210 215 220

Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro  
225 230 235 240

Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val  
245 250 255

Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala  
260 265 270

<210> 79

<211> 167

<212> PRT

<213> Homo sapiens

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<400> 79

Met Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly  
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Asn Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly  
20 25 30

Gly Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro  
35 40 45

Ile Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu  
50 55 60

Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn  
65 70 75 80

Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln  
85 90 95

Val Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr  
100 105 110

Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe  
115 120 125

Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly  
130 135 140

Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr  
145 150 155 160

Pro Thr Ser Cys Ser Arg Cys  
165

<210> 80

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (22)

<223> Xaa equals stop translation

<400> 80

Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala  
1 5 10 15

His Ser Gly Arg Ala Xaa  
20

<210> 81

MAILING ADDRESS OF SENDER

U.S. Patent No. 6,994,857

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Washington, D.C. 20001-4413

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<211> 733
<212> DNA
<213> Homo sapiens

<400> 81
gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg      60
aattcgaggg tgcaccgtca gtcttctctt tcccccaaa acccaaggac accctcatga      120
tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg      180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg      240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact      300
ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca acccccatcg      360
agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc      420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct      480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga      540
ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg      600
acaagagcag gtggcagcag gggAACgtct tctcatgctc cgtgatgcat gaggctctgc      660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc      720

gactctagag gat

<210> 82
<211> 5
<212> PRT
<213> Artificial sequence
<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors

<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any

<400> 82
Trp Ser Xaa Trp Ser
  1             5

<210> 83
<211> 86
<212> DNA

```

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<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 83
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60
cccgaatat ctgccatctc aattag 86

<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 84
gcggcaagct ttttgcaaag cctaggg 27

<210> 85
<211> 271
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 85
ctcgagattt ccccgaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
aaatatctgc catctcaatt agtcagcaac catagtcccc cccctaactc cgcccatccc 120
gcccctaact ccgccagtt ccgccattc tccgcccatt ggctgactaa ttttttttat 180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 86
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 86

```

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gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 87  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <221> primer\_bind  
 <223> primer useful for generation of a EGR/SEAP reporter construct

<400> 87  
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<210> 88  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <221> misc\_binding  
 <223> NF-KB binding site

<400> 88  
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<210> 89  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <221> primer\_bind  
 <223> forward primer useful for generation of a vector containing the  
 NF-KB promoter element

<400> 89  
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 ccattctcaat tag 73

<210> 90  
 <211> 256  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <221> misc\_feature  
 <223> Synthetic NF-KB/SV40 promoter

<400> 90  
 ctcgagggga ctttcccgga gactttccgg ggactttccg ggactttcca tctgccatct 60  
 caattagtca gcaaccatag tccgcgccct aactccgccc atccgcgccc taactccgcc 120  
 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180

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ggccgctcgc gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240

cttttgcaaa aagctt 256

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In the Claims

Col. 313, line 22, in claim 1(c), "amino and" should read -- amino --.

Col. 313, line 33, in claim 1(e), "or fragment thereof and albumin" should read -- or fragment thereof, and albumin --.

Col. 313, line 55, in claim 1(i), "proten" should read -- protein --.

Col. 316, line 17, in claim 22, "protein, or thereof" should read -- protein, or fragment thereof --.

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